

Gencore version 5.1.6.
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OM protein - nucleic search, using frame plus p2n model

Run on: September 17, 2004, 15:17:28 ; Search time 1 Seconds
(without alignments)

0.993 Million cell updates/sec

Perfect score: 1244

Sequence: 1 MMPKHCFLGLISPFITGVY.....YQPMLDRRSQRSEERCVBIP 231

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1 seqs, 2149 residues

Total number of hits satisfying chosen parameters: 2
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL:frame -p2n.mde1 -DEV:SOFT -Q=us-09 919-162f 6 -DB=us-09-728-911-1
-SUFFIX=pto -OUT=09919162-6v809728911-1.res -MINMATCH=0.1 -LOOPC1=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40_cdi -LIST=45
-DCALIGN=200 -THR SCORE=PCP -THR MAY=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-ODCFMT=pto -NORM=ext -HEARSIZE=00 -MINLEN=0 -MAXLEN=200000000 -NCPU=6
-NO_XLIPY=1 -NG SCORES=0 -LONGEXT=0 -XGAPOP=10 -YGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=5 -DELOP=6 -DELEXT=7
Database : us-09-728-911-1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Match	Length	DB	ID	Description
1	1244	100.0	2149	1	us-09-728-911-1	

ALIGNMENTS

RESULT 1
us-09-728-911-1

Alignment Scores:
Pred. No. : 0 Length: 2149
Score: 1244.00 Matches: 231
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

us-09-919-162f-6 (1-231) x us-09-728-911-1 (1-2149)

Qy 1 MetMetProLysHisCysSerLeuGlyPheLeuLeSerPhePheLeuThrGlyValAla 20